

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,106

DATE: 07/09/2001

TIME: 10:18:53

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Output Set: N:\CRF3\07092001\I869106.raw

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3 <110> APPLICANT: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
4   POQUET, Isabelle
5   GRUSS, Alexandra
6   BOLOTINE, Alexandre
7   SOROKINE, Alexei
9 <120> TITLE OF INVENTION: GRAM-POSITIVE BACTERIA DEPRIVED OF HtrA PROTEASIS
10  ACTIVITY, AND THEIR USES
12 <130> FILE REFERENCE: 45636-5048-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/869,106
C--> 15 <141> CURRENT FILING DATE: 2001-06-22
17 <150> PRIOR APPLICATION NUMBER: FR98/16462
18 <151> PRIOR FILING DATE: 1998-12-24
20 <150> PRIOR APPLICATION NUMBER: PCT/FR99/03270
21 <151> PRIOR FILING DATE: 1999-12-23
23 <160> NUMBER OF SEQ ID NOS: 2
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1740
29 <212> TYPE: DNA
30 <213> ORGANISM: Lactococcus lactis
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (230)..(1453)
36 <400> SEQUENCE: 1
37 aaacaagatg aaaacatgat ttatcaacat ttttttactt ttttccactt ttctgtggaa 60
39 aactttatta aaatatccac ttatcctcat taatttttag attatccaca aaaatgtgga 120
41 gaaactatat tagtttgatt tttgttacta ttaaggtatt attaagtgag agtagatata 180
43 attacatcat agaaatgcta caaagattaa taattgaaag gaattattt atg gca aaa 238
44                                     Met Ala Lys
45                                     1
47 gct aat ata gga aaa ttg cta tta aca ggt gtc gtg ggc gga gcc atc 286
48 Ala Asn Ile Gly Lys Leu Leu Leu Thr Gly Val Val Gly Gly Ala Ile
49      5      10      15
51 gca ctt gga gga agt gca atc tat caa agc act aca aat caa tcg gca 334
52 Ala Leu Gly Gly Ser Ala Ile Tyr Gln Ser Thr Thr Asn Gln Ser Ala
53 20      25      30      35
55 aat aat agt cgt tca aat aca act agt aca aag gtt agt aac gtt tcg 382
56 Asn Asn Ser Arg Ser Asn Thr Thr Ser Thr Lys Val Ser Asn Val Ser
57      40      45      50
59 gta aat gtc aat acc gat gtt acc tct gca att gaa aaa gtt tca aat 430
60 Val Asn Val Asn Thr Asp Val Thr Ser Ala Ile Glu Lys Val Ser Asn
61      55      60      65
63 tct gtc gtt tct gtt atg aat tat caa aaa gat aac tca caa agt agt 478
64 Ser Val Val Ser Val Met Asn Tyr Gln Lys Asp Asn Ser Gln Ser Ser
65 70      75      80
67 gac ttc agt tca att ttt ggt gga aat agc ggt tca agt tca tcg act 526
68 Asp Phe Ser Ser Ile Phe Gly Gly Asn Ser Gly Ser Ser Ser Ser Thr

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69      85      90      95
71 gat ggc tta cag ctt tct agt gaa ggc tct ggt gtc atc tac aaa aaa 574
72 Asp Gly Leu Gln Leu Ser Ser Glu Gly Ser Gly Val Ile Tyr Lys Lys
73 100      105      110      115
75 tct ggt ggt gat gcc tac gtt gta act aac tac cac gtt att gct ggt 622
76 Ser Gly Gly Asp Ala Tyr Val Val Thr Asn Tyr His Val Ile Ala Gly
77      120      125      130
79 aat agc tca ctt gat gtt ctg ctt tct ggt gga caa aaa gtc aaa gat 670
80 Asn Ser Ser Leu Asp Val Leu Leu Ser Gly Gly Gln Lys Val Lys Asp
81      135      140      145
83 tct gtg gtt ggt tat gat gaa tac aca gac ctt gct gtt ctt aaa atc 718
84 Ser Val Val Gly Tyr Asp Glu Tyr Thr Asp Leu Ala Val Leu Lys Ile
85      150      155      160
87 agt tct gaa cat gtc aaa gat gtg gcg aca ttc gct gat tct agt aaa 766
88 Ser Ser Glu His Val Lys Asp Val Ala Thr Phe Ala Asp Ser Ser Lys
89      165      170      175
91 tta aca att ggt gaa cct gcc att gcc gtt gcc tca cct tta ggt agt 814
92 Leu Thr Ile Gly Glu Pro Ala Ile Ala Val Gly Ser Pro Leu Gly Ser
93 180      185      190      195
95 caa ttt gca aac acc gca act gaa gga att tta tct gca aca agc cgt 862
96 Gln Phe Ala Asn Thr Ala Thr Glu Gly Ile Leu Ser Ala Thr Ser Arg
97      200      205      210
99 caa gtg act ttg acc caa gaa aat ggt caa aca act aat atc aat gca 910
100 Gln Val Thr Leu Thr Gln Glu Asn Gly Gln Thr Thr Asn Ile Asn Ala
101      215      220      225
103 att caa aca gat gct gcc att aac cct ggt aac tct gga ggg gct ttg 958
104 Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser Gly Gly Ala Leu
105      230      235      240
107 att aat att gaa gga caa gtt att gga att act caa agt aaa att aca 1006
108 Ile Asn Ile Glu Gly Gln Val Ile Gly Ile Thr Gln Ser Lys Ile Thr
109      245      250      255
111 aca act gaa gat ggt tct act tct gtc gaa ggt tta gga ttt gcg att 1054
112 Thr Thr Glu Asp Gly Ser Thr Ser Val Glu Gly Leu Gly Phe Ala Ile
113 260      265      270      275
115 cct tct aat gat gtc gta aat atc att aat aaa ctt gaa gat gat ggt 1102
116 Pro Ser Asn Asp Val Val Asn Ile Ile Asn Lys Leu Glu Asp Asp Gly
117      280      285      290
119 aag att tca cgc cct gct tta ggt atc cga atg gtt gac ctt tca caa 1150
120 Lys Ile Ser Arg Pro Ala Leu Gly Ile Arg Met Val Asp Leu Ser Gln
121      295      300      305
123 tta tca aca aat gac agt tct caa ttg aaa tta cta agc agt gta aca 1198
124 Leu Ser Thr Asn Asp Ser Ser Gln Leu Lys Leu Leu Ser Ser Val Thr
125      310      315      320
127 ggt ggg gtt gtt gtt tac tcc gtc caa tct gga ctt cct gct gcc tca 1246
128 Gly Gly Val Val Val Tyr Ser Val Gln Ser Gly Leu Pro Ala Ala Ser
129      325      330      335
131 gct ggt ttg aaa gct gga gat gta att aca aag gtt ggc gat aca gca 1294
132 Ala Gly Leu Lys Ala Gly Asp Val Ile Thr Lys Val Gly Asp Thr Ala
133 340      345      350      355

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135 gta acc tct tca aca gac ttg caa agt gct ctt tac tca cac aat atc 1342
136 Val Thr Ser Ser Thr Asp Leu Gln Ser Ala Leu Tyr Ser His Asn Ile
137          360          365          370
139 aat gat aca gta aaa gtt act tat tat cgt gat ggt aaa tca aat aca 1390
140 Asn Asp Thr Val Lys Val Thr Tyr Tyr Arg Asp Gly Lys Ser Asn Thr
141          375          380          385
143 gca gat gtt aaa ctt tct aaa tca acc agt gac tta gaa aca agc agt 1438
144 Ala Asp Val Lys Leu Ser Lys Ser Thr Ser Asp Leu Glu Thr Ser Ser
145          390          395          400
147 cca tct tct tct aat taataactta ataatttaaat aaaagtcttc tgtaaataga 1493
148 Pro Ser Ser Ser Asn
149          405
151 aggctttttt cataactaaag tctgaaattt ttaaaaaataa taaatttcca tttttctttt 1553
153 attgatttat ggtaaaataa agttaagcat gaaaatttta ctttacttag aagccgaaca 1613
155 atttttgagt cattcaggaa ttggtcgtgc aatgaaacat caacaacgcg cccttgattt 1673
157 aatgggcatt gactggacaa aaaatcctga ggatgattac gatatcctcc atttaaatac 1733
159 ttatggc 1740
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 408
164 <212> TYPE: PRT
165 <213> ORGANISM: Lactococcus lactis
167 <400> SEQUENCE: 2
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169 1 5 10 15
171 Gly Ala Ile Ala Leu Gly Gly Ser Ala Ile Tyr Gln Ser Thr Thr Asn
172 20 25 30
174 Gln Ser Ala Asn Asn Ser Arg Ser Asn Thr Thr Ser Thr Lys Val Ser
175 35 40 45
177 Asn Val Ser Val Asn Val Asn Thr Asp Val Thr Ser Ala Ile Glu Lys
178 50 55 60
180 Val Ser Asn Ser Val Val Ser Val Met Asn Tyr Gln Lys Asp Asn Ser
181 65 70 75 80
183 Gln Ser Ser Asp Phe Ser Ser Ile Phe Gly Gly Asn Ser Gly Ser Ser
184 85 90 95
186 Ser Ser Thr Asp Gly Leu Gln Leu Ser Ser Glu Gly Ser Gly Val Ile
187 100 105 110
189 Tyr Lys Lys Ser Gly Gly Asp Ala Tyr Val Val Thr Asn Tyr His Val
190 115 120 125
192 Ile Ala Gly Asn Ser Ser Leu Asp Val Leu Leu Ser Gly Gly Gln Lys
193 130 135 140
195 Val Lys Asp Ser Val Val Gly Tyr Asp Glu Tyr Thr Asp Leu Ala Val
196 145 150 155 160
198 Leu Lys Ile Ser Ser Glu His Val Lys Asp Val Ala Thr Phe Ala Asp
199 165 170 175
201 Ser Ser Lys Leu Thr Ile Gly Glu Pro Ala Ile Ala Val Gly Ser Pro
202 180 185 190
204 Leu Gly Ser Gln Phe Ala Asn Thr Ala Thr Glu Gly Ile Leu Ser Ala
205 195 200 205
207 Thr Ser Arg Gln Val Thr Leu Thr Gln Glu Asn Gly Gln Thr Thr Asn

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208      210      215      220
210 Ile Asn Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser Gly
211 225      230      235      240
213 Gly Ala Leu Ile Asn Ile Glu Gly Gln Val Ile Gly Ile Thr Gln Ser
214      245      250      255
216 Lys Ile Thr Thr Thr Glu Asp Gly Ser Thr Ser Val Glu Gly Leu Gly
217      260      265      270
219 Phe Ala Ile Pro Ser Asn Asp Val Val Asn Ile Ile Asn Lys Leu Glu
220      275      280      285
222 Asp Asp Gly Lys Ile Ser Arg Pro Ala Leu Gly Ile Arg Met Val Asp
223      290      295      300
225 Leu Ser Gln Leu Ser Thr Asn Asp Ser Ser Gln Leu Lys Leu Leu Ser
226 305      310      315      320
228 Ser Val Thr Gly Gly Val Val Val Tyr Ser Val Gln Ser Gly Leu Pro
229      325      330      335
231 Ala Ala Ser Ala Gly Leu Lys Ala Gly Asp Val Ile Thr Lys Val Gly
232      340      345      350
234 Asp Thr Ala Val Thr Ser Ser Thr Asp Leu Gln Ser Ala Leu Tyr Ser
235      355      360      365
237 His Asn Ile Asn Asp Thr Val Lys Val Thr Tyr Tyr Arg Asp Gly Lys
238      370      375      380
240 Ser Asn Thr Ala Asp Val Lys Leu Ser Lys Ser Thr Ser Asp Leu Glu
241 385      390      395      400
243 Thr Ser Ser Pro Ser Ser Ser Asn
244      405

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**VERIFICATION SUMMARY**

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date